

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

OM nucleic - nucleic search, using sw model					
Run on:	July 13, 2003, 21:41:37 ; search time 1093 Seconds (Without alignments) 3488.076 Million cell updates/sec				
title:	US-09-661-658B-2				
Perfect score:	131				
Sequence:	1 ggcttagataaggtaactt.....atgcctaacgactatccct 131				
Scoring table:	IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0					
Searched:	2054640 seqs, 14551402878 residues				
Total number of hits satisfying chosen parameters:	4109280				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Listing first 45 summaries					
Database :					
1: gb_ba:*					
2: gb_htg:*					
3: qb_in:*					
4: qb_on:*					
5: qb_ov:*					
6: qb_pdt:*					
7: qb_ph:*					
8: qb_pl:*					
9: qb_pr:*					
10: qb_ro:*					
11: qb_sts:*					
12: qb_sy:*					
13: qb_un:*					
14: qb_vl:*					
15: em_da:*					
16: em_fun:*					
17: em_hum:*					
18: em_in:*					
19: em_ml:*					
20: em_on:*					
21: em_or:*					
22: em_lov:*					
23: em_par:*					
24: em_ph:*					
25: em_pl:*					
26: em_ro:*					
27: em_sts:*					
28: em_vl:*					
29: em_un:*					
30: em_htg_hum:*					
31: em_htg_inv:*					
32: em_htg_other:*					
33: em_htg_mus:*					
34: em_htg_pln:*					
35: em_htg_rod:*					
36: em_htg_mam:*					
37: em_htg_vrt:*					
38: em_sy:*					
39: em_htgo_hum:*					
40: em_htgo_mus:*					
41: em_htgo_other:*					

Pred. No. is the number of results predicted by chance to have a

ALIGNMENTS

RESULT 1					
AX379337	LOCUS	AX379337	DEFINITION	Sequence 2 from Patent WO0196541.	DNA
DEFINITION	Sequence 2 from Patent WO0196541.				Linear
ACCESSION	AX379337	AX379337	ACCESSION		PAT 18-MAR-2002
VERSION	AX379337.1	GI:19575177	VERSION		
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					

Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
Allosterically regulated ribozymes
Patent: WO 0196541-A 20-DEC-2001;

FEATURES	BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)	KEYWORDS
SOURCE	LOCATION/QUALIFIERS	SOURCE
BASE COUNT	37 a 32 c 24 g 38 t	ORGANISM synthetic construct.
ORIGIN	/note="Engineered Aptazyme"	REFERENCE 1. .131 /organism="synthetic construct" /db:xref="taxon:32630"
Query Match	100.0%; Score 131; DB 6; Length 131;	AUTHORS Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M.,
Best Local Similarity	100.0%; Pred. No. 9; 7e-34; Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TITLE Sooter, L., Davidson, E., Cox, J.C. and Reidel, T.
DEFINITION Sequence 5 from Patent WO1965411.	ACCESSTION AX379340	JOURNAL Regulatable, catalytically active nucleic acids
PATENT: WO 196541-A 5 20-DEC-2001;	VERSION AX379340.1	Patent: WO 0196559-A 5 20-DEC-2001;
KEYWORDS	KEYWORD SOURCE ORGANISM	Board of Regents, The University of Texas System (US)
synthetic construct.	synthetic construct.	Location/Qualifiers
REFERENCE	1. .131	1. .131
AUTHORS	Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M., Sooter, L., Davidson, E., Cox, J.C. and Reidel, T.	1. .131
TITLE	AllostERICALLY regulated ribozymes	REGULATORY ELEMENTS
JOURNAL	Patent: WO 196541-A 5 20-DEC-2001;	Regulatable, catalytically active nucleic acids
FEATURES	BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)	Board of Regents, The University of Texas System (US)
BASE COUNT	37 a 32 c 24 g 36 t	Location/Qualifiers
ORIGIN	/note="Engineered Aptazyme" /db:xref="taxon:32630"	1. .131
Query Match	97.3%; Score 127.4; DB 6; Length 131;	RESULT 4
Best Local Similarity	97.7%; Pred. No. 1.6e-32; Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	AX427121
DEFINITION	Sequence 21 from Patent WO0196559.	LOCUS AX427121
ACCESSTION	AX427121	DEFINITION 128 bp
VERSION	AX427121.1	VERSION PAT 18-JUN-2002
KEYWORDS	KEYWORD SOURCE ORGANISM	KEYWORD SOURCE ORGANISM
synthetic construct.	synthetic construct.	synthetic construct.
REFERENCE	1. .128	REFERENCE 1. .128
AUTHORS	Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M., Sooter, L., Davidson, E., Cox, J.C. and Reidel, T.	AUTHORS Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M., Sooter, L., Davidson, E., Cox, J.C. and Reidel, T.
TITLE	Regulatable, catalytically active nucleic acids	TITLE Regulatable, catalytically active nucleic acids
JOURNAL	Patent: WO 0196559-A 21 20-DEC-2001;	JOURNAL Patent: WO 0196559-A 21 20-DEC-2001;
FEATURES	Board of Regents, The University of Texas System (US)	FEATURES Board of Regents, The University of Texas System (US)
BASE COUNT	36 a 32 c 23 g 37 t	Location/Qualifiers
ORIGIN	/note="Oligonucleotide" /db:xref="taxon:32630"	1. .128
Query Match	93.9%; Score 123; DB 6; Length 128;	Query Match
Best Local Similarity	100.0%; Pred. No. 5.1e-31; Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	93.9%; Score 123; DB 6; Length 128;
DEFINITION	Sequence 5 from Patent WO196559.	Best Local Similarity
ACCESSTION	AX427105	DEFINITION Sequence 5 from Patent WO196559.
VERSION	AX427105.1	ACCESSTION AX427105
RESULT 3	131 bp	VERSION AX427105.1
LOCUS	DNA	LINEAR
DEFINITION	Linear	PAT 18-JUN-2002
ACCESSTION	AX427105	GI:21530488
VERSION	AX427105.1	131 CTT 131

Db	126 CTT 128	RESULT 5	AX427102	Sequence 2 from Patent WO196559.	130 bp	DNA	linear	PAT 18-JUN-2002
DEFINITION	LOCUS	ACCESSION	JOURNAL	KEYWORDS	FEATURES	SOURCE	ORGANISM	
AUTHORS	Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	Regulatable, catalytically active nucleic acids	Patent: WO 0196559-A 2 20-DEC-2001; Board of Regents, The University of Texas System (US)	synthetic construct.	artificial sequences.			
TITLE								
VERSION	AX427102.1	GI:21530485						
KEYWORDS								
SOURCE								
ORGANISM								
ARTICLE								
BASE COUNT	37 a	32 c	24 g	37 t	BASE COUNT	36 a	32 c	24 g
ORIGIN					ORIGIN			
Query Match	90.8%	Score 119;	DB 6;	Length 130;	Query Match	91.7%	Score 107;	DB 6;
Best Local Similarity	99.2%	Pred. No. 1.2e-29;			Best Local Similarity	98.5%	Pred. No. 1.4e-25;	Length 129;
Matches	130;	Conservative 0;	Mismatches	0;	Matches	129;	Conservative 0;	
Indels	1;	Gaps	1;		Indels	2;	Gaps	2;
Db					Db			
QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAAACGGGAACCTCTCTAGTAGA	60	QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAAACGGGAACCTCTCTAGTAGA	60			
Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAAACGGGAACCTCTCTAGTAGA	60	Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAAACGGGAACCTCTCTAGTAGA	60			
QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAGATAATTGCTAAC	120	QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAGATAATTGCTAAC	119			
Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAGATAATTGCTAAC	120	Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAGATAATTGCTAAC	119			
QY	121 GACTATCCCT 131		QY	121 GACTATCCCT 131				
Db	120 GACTATCCCT 130		Db	120 GACTATCCCT 130				
RESULT 6	AX427122	Sequence 22 from Patent WO196559.	133 bp	DNA	linear	PAT 18-JUN-2002	BASE COUNT	36 a
DEFINITION	LOCUS	ACCESSION	VERSION		ORIGIN		BASE COUNT	36 a
AUTHORS	Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	Regulatable, catalytically active nucleic acids	Patent: WO 0196559-A 22 20-DEC-2001; Board of Regents, The University of Texas System (US)	synthetic construct.	artificial sequences.		BASE COUNT	36 a
TITLE								
VERSION	AX427122.1	GI:21530505						
KEYWORDS								
SOURCE								
ORGANISM								
ARTICLE								
BASE COUNT	37 a	33 c	25 g	38 t	BASE COUNT	36 a	32 c	24 g
ORIGIN					ORIGIN			
Query Match	83.2%	Score 109;	DB 6;	Length 133;	Query Match	98.5%	Score 109;	DB 6;
Best Local Similarity	98.5%	Pred. No. 2.9e-26;			Best Local Similarity	98.5%	Pred. No. 2.9e-26;	Length 131;
Matches	131;	Conservative 0;	Mismatches	0;	Matches	131;	Conservative 0;	
Indels	2;	Gaps	2;		Indels	2;	Gaps	2;
Db					Db			
QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60	QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60			
Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60	Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60			
QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	118	QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	120			
Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	118	Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	120			
QY	121 GACTATCCCT 131		QY	121 GACTATCCCT 133				
Db	121 GACTATCCCT 133		Db	121 GACTATCCCT 133				
RESULT 7	AX427124	Sequence 24 from Patent WO196559.	129 bp	DNA	linear	PAT 18-JUN-2002	BASE COUNT	36 a
DEFINITION	LOCUS	ACCESSION	VERSION		ORIGIN		BASE COUNT	36 a
AUTHORS	Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	Regulatable, catalytically active nucleic acids	Patent: WO 0196559-A 24 20-DEC-2001; Board of Regents, The University of Texas System (US)	synthetic construct.	artificial sequences.		BASE COUNT	36 a
TITLE								
VERSION	AX427124.1	GI:21530507						
KEYWORDS								
SOURCE								
ORGANISM								
ARTICLE								
BASE COUNT	37 a	32 c	24 g	37 t	BASE COUNT	36 a	32 c	24 g
ORIGIN					ORIGIN			
Query Match	90.8%	Score 119;	DB 6;	Length 130;	Query Match	91.7%	Score 107;	DB 6;
Best Local Similarity	99.2%	Pred. No. 1.2e-29;			Best Local Similarity	98.5%	Pred. No. 1.4e-25;	Length 129;
Matches	130;	Conservative 0;	Mismatches	0;	Matches	129;	Conservative 0;	
Indels	1;	Gaps	1;		Indels	2;	Gaps	2;
Db					Db			
QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60	QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60			
Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60	Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60			
QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	120	QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	118			
Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	120	Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	118			
QY	121 GACTATCCCT 131		QY	121 GACTATCCCT 133				
Db	121 GACTATCCCT 133		Db	121 GACTATCCCT 133				
RESULT 8	AX427123	Sequence 23 from Patent WO196559.	119 bp	DNA	linear	PAT 18-JUN-2002	BASE COUNT	36 a
DEFINITION	LOCUS	ACCESSION	VERSION		ORIGIN		BASE COUNT	36 a
AUTHORS	Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	Regulatable, catalytically active nucleic acids	Patent: WO 0196559-A 23 20-DEC-2001; Board of Regents, The University of Texas System (US)	synthetic construct.	artificial sequences.		BASE COUNT	36 a
TITLE								
VERSION	AX427123.1	GI:21530506						
KEYWORDS								
SOURCE								
ORGANISM								
ARTICLE								
BASE COUNT	37 a	33 c	25 g	38 t	BASE COUNT	36 a	32 c	24 g
ORIGIN					ORIGIN			
Query Match	83.2%	Score 109;	DB 6;	Length 133;	Query Match	98.5%	Score 109;	DB 6;
Best Local Similarity	98.5%	Pred. No. 2.9e-26;			Best Local Similarity	98.5%	Pred. No. 2.9e-26;	Length 131;
Matches	131;	Conservative 0;	Mismatches	0;	Matches	131;	Conservative 0;	
Indels	2;	Gaps	2;		Indels	2;	Gaps	2;
Db					Db			
QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60	QY	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60			
Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60	Db	1 GCCTGAGTATAAGGTGACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGA	60			
QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	120	QY	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	118			
Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	120	Db	61 CAATCCGGTGTAAATTATACCAAGATCGCTTGATGCCCTGGCAG-TAAATGCTAAC	118			
QY	121 GACTATCCCT 131		QY	121 GACTATCCCT 133				
Db	121 GACTATCCCT 133		Db	121 GACTATCCCT 133				

BASE COUNT 30 a /note="Oligonucleotide"
ORIGIN 32 c 24 g 33 t

FEATURES Board of Regents, The University of Texas System (US)
source Location/Qualifiers 1..115
Query Match /organism="synthetic construct"
Best Local Similarity 66.4%; Score 87; DB 6; Length 119;
Matches 119; Conservative 0; Mismatches 0; Indels 12; Gaps 2;

QY 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60
Db 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60

QY 61 CAATCCCGCTAAATTATACACGATCGCTGTAGGCCCTGGCAGATAATGCCTAAC 120
Db 61 CAATCCCGCTGC-----ATACAGCATCGCTGTAGGCCCTGGCAG-----GCCTAAC 108

QY 121 GACTATCCCT 131
Db 109 GACTATCCCT 119

RESULT 9

LOCUS AX427126 Sequence 26 from Patent WO0196559. 117 bp DNA linear PAT 18-JUN-2002

DEFINITION AX427126 VERSION GI:21530509

ACCESSION KEYWORDS . synthetic construct.

TITLE Patent: WO 0196559-A 26 20-DEC-2001; Board of Regents, The University of Texas System (US)

SOURCE FEATURES .
1. .117
1. /Organism="synthetic construct"
/db_xref="taxon:32630"

REFERENCE ORIGIN 30 a /note="Oligonucleotide" 31 c 23 g 33 t

BASE COUNT 30 a /note="Oligonucleotide"
ORIGIN 32 c 24 g 33 t

Query Match Best Local Similarity 66.0%; Score 86.4; DB 6; Length 117; Matches 107; Conservative 0; Mismatches 11; Indels 13; Gaps 1;

QY 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60
Db 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60

QY 61 CAATCCCGCTAAATTATACACGATCGCTGTAGGCCCTGGCAGATAATGCCTAAC 120
Db 61 CAATCCCGCTGC-----ATACAGCATCGCTGTAGGCCCTGGCAGCTAAC 113

RESULT 10

LOCUS AX427125 Sequence 25 from Patent WO0196559. 115 bp DNA linear PAT 18-JUN-2002

DEFINITION AX427125 VERSION AX427125.1 GI:21530508

ACCESSION KEYWORDS . synthetic construct.

SOURCE ORIGIN 30 a /note="Oligonucleotide" 31 c 23 g 33 t

REFERENCE ORIGIN 32 c 24 g 33 t

BASE COUNT 30 a /note="Oligonucleotide"
ORIGIN 30 c 22 g 33 t

FEATURES Board of Regents, The University of Texas System (US)
source Location/Qualifiers 1..115
Query Match /organism="synthetic construct"
Best Local Similarity 63.7%; Score 83.4; DB 6; Length 115;
Matches 102; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60
Db 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60

QY 61 CAATCCCGCTAAATTATACACGATCGCTGTAGGCCCTGGCAGATAATGCCTAAC 111
Db 61 CAATCCCG-----TATACAGCATCGCTGTAGGCCCTGGCAGCTAAC 103

RESULT 11

LOCUS AX427131 Sequence 31 from Patent WO0196559. 122 bp DNA linear PAT 18-JUN-2002

DEFINITION AX427131 VERSION GI:21530514

ACCESSION KEYWORDS . synthetic construct.

TITLE Patent: WO 0196559-A 31 20-DEC-2001; Board of Regents, The University of Texas System (US)

SOURCE FEATURES .
1. .122
1. /Organism="synthetic construct"
/db_xref="taxon:32630"

REFERENCE ORIGIN 30 a /note="Oligonucleotide" 31 c 23 g 33 t

BASE COUNT 37 a /note="Oligonucleotide"
ORIGIN 36 c 25 g 34 t

Query Match Best Local Similarity 62.7%; Score 82.2; DB 6; Length 122; Matches 109; Conservative 0; Mismatches 11; Indels 9; Gaps 1;

QY 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60
Db 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60

QY 61 CAATCCCGCTAAATTATACACGATCGCTGTAGGCCCTGGCAGATAATGCCTAAC 120
Db 61 CAATCCCGCTGC-----ATACAGCATCGCTGTAGGCCCTGGCAGCTAAC 111

RESULT 12

LOCUS AX427129 Sequence 29 from Patent WO0196559. 107 bp DNA linear PAT 18-JUN-2002

DEFINITION AX427129 VERSION AX427129.1 GI:21530512

ACCESSION KEYWORDS . synthetic construct.

SOURCE ORIGIN 30 a /note="Oligonucleotide" 31 c 23 g 33 t

REFERENCE ORIGIN 32 c 24 g 33 t

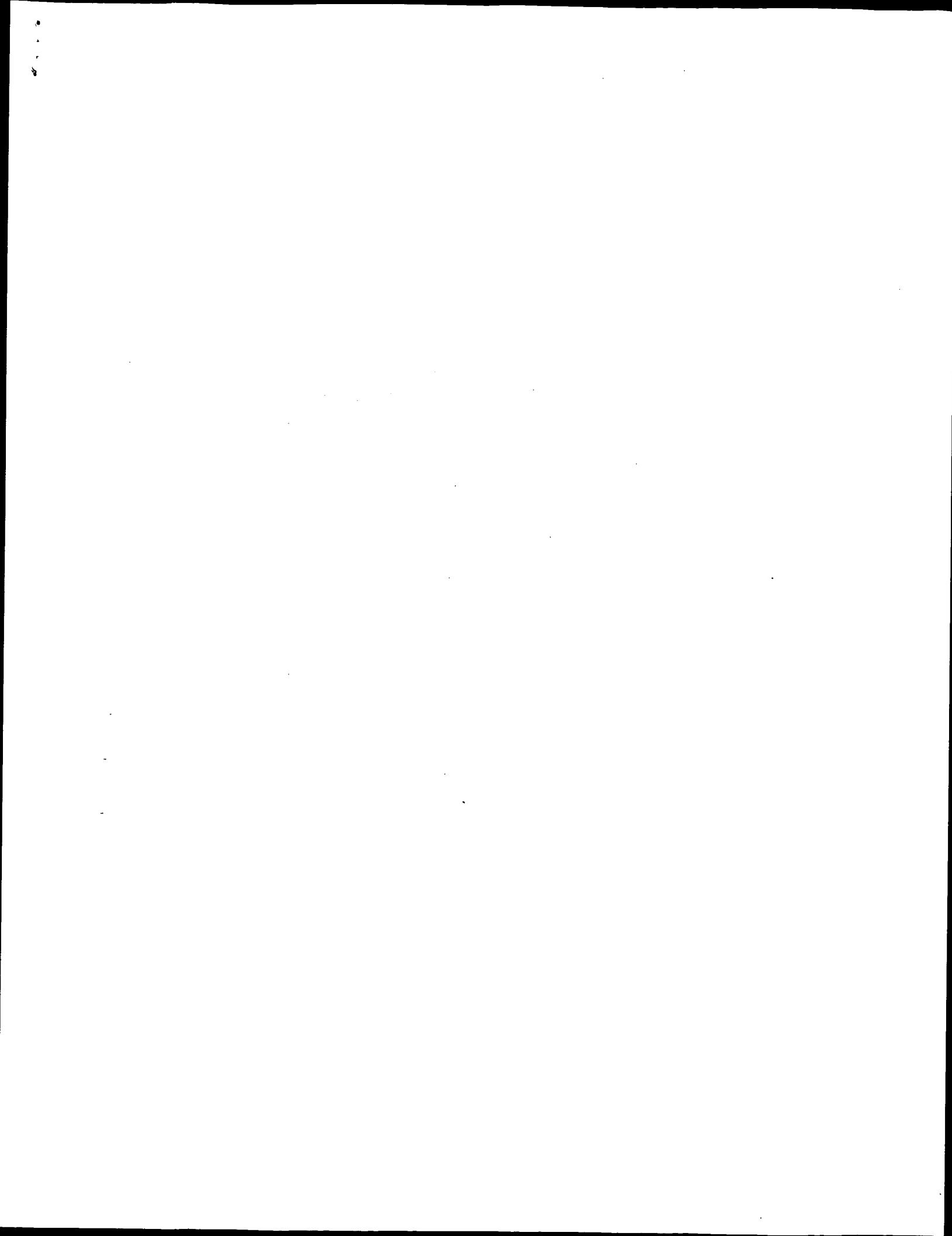
BASE COUNT 30 a /note="Oligonucleotide"
ORIGIN 30 c 22 g 33 t

FEATURES Board of Regents, The University of Texas System (US)
source Location/Qualifiers 1..115
Query Match /organism="synthetic construct"
Best Local Similarity 63.7%; Score 83.4; DB 6; Length 115;
Matches 102; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60
Db 1 GCCTGAGTATAAGGTGACTTATCTGATCTAACACGGGAACCTCTAGTA 60

QY 61 CAATCCCGCTAAATTATACACGATCGCTGTAGGCCCTGGCAGATAATGCCTAAC 111
Db 61 CAATCCCGCTGC-----TATACAGCATCGCTGTAGGCCCTGGCAGCTAAC 103

	REFERENCE	1
AUTHORS	Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE	Regulatable, catalytically active nucleic acids	Regulatable, catalytically active nucleic acids
JOURNAL	Patent: WO 0196559-A 29 20-DEC-2001; Board of Regents, The University of Texas System (US)	Patent: WO 0196559-A 30 20-DEC-2001; Board of Regents, The University of Texas System (US)
FEATURES	/note="Oligonucleotide"	/note="Oligonucleotide"
BASE COUNT	31 a 28 c 19 g 29 t	31 a 28 c 19 g 31 t
ORIGIN		
Query Match	62.1%; Score 81.4; DB 6; Length 107;	60.9%; Score 79.8; DB 6; Length 107;
Best Local Similarity	97.28%; Pred. No. 6.6e-17;	96.3%; Pred. No. 2.3e-16;
Matches	104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;	103; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY	27 GATACATCTAACGGGAAACCTCTAGTAGACATCCGGCTTAATT-ATACAGC 85	27 GTAATCTATCAACGGGAAACCTCTAGTAGACATCCGGCTTAATT ATACAGC 85
Db	1 GATACATCTAACGGGAAACCTCTAGTAGACATCCGGCTTAATTGATACAGC 60	1 GATACATCTAACGGGAAACCTCTAGTAGACATCCGGCTTAATTGATACAGC 60
QY	86 ATCGTCTGTAGGCCCTGGCAG-ATAATGCTAAGACTATCCCT 131	86 ATCGTCTGTAGGCCCTGGCAG-ATAATGCTAAGACTATCCCT 131
Db	61 ATCGTCTGTAGGCCCTGGCAG-ATAATGCTAAGACTATCCCT 107	61 ATCGTCTGTAGGCCCTGGCAG-ATAATGCTAAGACTATCCCT 107
RESULT 13		
LOCUS	AX427116	AX427116
DEFINITION	Sequence 16 from Patent WO0196559.	122 bp DNA linear PAT 18-JUN-2002
ACCESSION	AX427116	GI:21530499
VERSION	AX427116.1	
KEYWORDS		
SOURCE		
ORGANISM	synthetic construct.	synthetic construct.
ARTIFICIAL	artificial sequences.	artificial sequences.
REFERENCE	1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
AUTHORS	Title Regulatable, catalytically active nucleic acids	Title Regulatable, catalytically active nucleic acids
TITLE	Patent: WO 0196559-A 16 20-DEC-2001;	Patent: WO 0196559-A 16 20-DEC-2001;
JOURNAL	Board of Regents, The University of Texas System (US)	Board of Regents, The University of Texas System (US)
FEATURES	/note="Organism="synthetic construct"	/note="Organism="synthetic construct"
source	1.-122 /note="Organism="synthetic construct"	1.-122 /note="Organism="synthetic construct"
BASE COUNT	34 a 29 c 24 g 35 t	34 a 29 c 24 g 35 t
ORIGIN		
Query Match	61.5%; Score 80.6; DB 6; Length 122;	59.8%; Score 78.4; DB 6; Length 510;
Best Local Similarity	82.4%; Pred. No. 1.2e-16;	98.8%; Pred. No. 7.7e-16;
Matches	108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;	79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCTCTGAGTATAGGTGACTTATCTGTTCTAACGGGAACCTCTAGTAGA 60	1 GCTCTGAGTATAGGTGCTTATCTGTTCTAACGGGAACCTCTAGTAGA 60
Db	1 GCTCTGAGTATAGGTGACTTATCTGTTCTAACGGGAACCTCTAGTAGA 60	341 GCTCTGAGTATAGGTGACTTATCTGTTCTAACGGGAACCTCTAGTAGA 400
QY	61 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 120	61 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 120
Db	61 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 111	401 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 420
QY	121 GACTATCCCT 131	
Db	112 GACTATCCCT 122	
RESULT 14		
LOCUS	AX427130	AX427130
DEFINITION	Sequence 30 from Patent WO0196559.	107 bp DNA linear PAT 18-JUN-2002
ACCESSION	AX427130	
VERSION	AX427130.1	GI:21530513
KEYWORDS		
SOURCE		
ORGANISM	synthetic construct.	synthetic construct.
FEATURES		
REFERENCE	1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.	1 Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
AUTHORS	Title Regulatable, catalytically active nucleic acids	Title Regulatable, catalytically active nucleic acids
TITLE	Patent: WO 0196559-A 30 20-DEC-2001;	Patent: WO 0196559-A 30 20-DEC-2001;
JOURNAL	Board of Regents, The University of Texas System (US)	Board of Regents, The University of Texas System (US)
FEATURES	/note="Organism="synthetic construct"	/note="Organism="synthetic construct"
source	/db:xref="taxon:32630"	/db:xref="taxon:32630"
BASE COUNT	153 a 80 c 109 g 168 t	153 a 80 c 109 g 168 t
ORIGIN		
Query Match	59.8%; Score 78.4; DB 6; Length 510;	59.8%; Score 78.4; DB 6; Length 510;
Best Local Similarity	98.8%; Pred. No. 7.7e-16;	98.8%; Pred. No. 7.7e-16;
Matches	79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCTCTGAGTATAGGTGCTTATCTGTTCTAACGGGAACCTCTAGTAGA 60	1 GCTCTGAGTATAGGTGCTTATCTGTTCTAACGGGAACCTCTAGTAGA 60
Db	1 GCTCTGAGTATAGGTGCTTATCTGTTCTAACGGGAACCTCTAGTAGA 60	341 GCTCTGAGTATAGGTGACTTATCTGTTCTAACGGGAACCTCTAGTAGA 400
QY	61 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 120	61 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 120
Db	61 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 111	401 CAATCCGGTCTAAATATACACCATCTCTGATGCCCTGGCAGATAATGCCAAC 420
SEARCH COMPLETED	Search completed: July 13, 2003, 22:53:39	Job time : 1094 secs



PT assays for detecting the presence of ligands or activation of an effector of RCANA
 PT XX
 PS Example 1; Page 40; 126pp; English.
 CC The present invention relates to regulatable, catalytically active nucleic acids (RNAs), which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the construction of an RCANA.
 SQ Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;
 Query Match 100 0%; Score 131; DB 24; Length 131;
 Best Local Similarity 100 0%; Pred. No. 5.4e-38;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCCTGAGTATAAGGTGACTATACATGTAATCTAATACGGGAACCTCTAGTAGA 60
 Db 1 GCCTGAGTATAAGGTGACTATACATGTAATCTAATACGGGAACCTCTAGTAGA 60
 Qy 61 CAATCCGGTGCTAAATTATACCAGCATCCTGATGCCCTGGCAGATAATGCCAAC 120
 Db 61 CAATCCGGTGCTAAATTATACCAGCATCCTGATGCCCTGGCAGATAATGCCAAC 120
 Qy 121 GACTATCCCT 131
 Db 121 GACTATCCCT 131
 RESULT 2
 AAL43049
 ID AAL43049 standard; DNA; 131 BP.
 AC AAL43049;
 XX
 DT 25-SEP-2002 (first entry)
 DE Regulatable, catalytically active nucleic acid construction oligo #8.
 KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;
 gene therapy; ds.
 XX OS Synthetic.
 XX
 WO200196559-A2.
 PN
 PR 14-JUN-2001; 2001WO-US19302.
 PR 15-JUN-2000; 2000US-212097P.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
 PI Davidson E, Cox JC, Reidel T;
 XX DR WPI; 2002-122216/16.
 PT New regulatable, catalytically active nucleic acids (RNA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA.
 PS Example 5; Page 68; 126pp; English.

The present invention relates to regulatable, catalytically active nucleic acids (RNAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the

CC construction of an RCANA.
 XX SQ Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;
 Query Match 100 0%; Score 131; DB 24; Length 131;
 Best Local Similarity 100 0%; Pred. No. 5.4e-38;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCCTGAGTATAAGGTGACTATACATGTAATCTAATACGGGAACCTCTAGTAGA 60
 Db 1 GCCTGAGTATAAGGTGACTATACATGTAATCTAATACGGGAACCTCTAGTAGA 60
 Qy 61 CAATCCGGTGCTAAATTATACCAGCATCCTGATGCCCTGGCAGATAATGCCAAC 120
 Db 61 CAATCCGGTGCTAAATTATACCAGCATCCTGATGCCCTGGCAGATAATGCCAAC 120
 Qy 121 GACTATCCCT 131
 Db 121 GACTATCCCT 131
 RESULT 3
 ID ABNU3045
 ID ABNU3045 standard; DNA; 131 BP.
 AC ABNU3045;
 XX
 DT 16-AUG-2002 (first entry)
 DE Aptazyme construct oligonucleotide GpIth1P6.131.
 XX Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; GpIth1P6.131; ss.
 OS Unidentified.
 XX
 PN WO200196541-A2.
 XX PD 20-DEC-2001.
 XX PF 15-JUN-2001; 2001WO-US19119.
 XX PR 15-JUN-2000; 2000US-0661658.
 XX PA (TEXA) UNIV TEXAS.
 XX DR Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
 PT Davidson E, Cox JC, Reidel T;
 XX DR WPI; 2002-090203/12.
 PT Aptazyme construct for detecting the presence of ligands, comprises a regulatable Group I intron aptamer oligonucleotide with a regulatory domain, and modulates their kinetic parameters in response to an effector.
 XX PS Claim 7; Page 30; 42pp; English.
 XX
 CC The sequence represents an oligonucleotide used in the invention in the construction of a group I regulatable aptazyme. The invention relates to a novel aptazyme construct comprising a regulatable Group I intron aptamer oligonucleotide sequence having an allosterically regulatable regulatory domain, where the kinetic parameters of the aptazyme on a target gene vary in response to the interaction of an allosteric effector molecule with the regulatory domain, and the intron splicing reaction occurs in vitro. The aptazyme is useful: (1) in assays to detect the presence of ligands or to detect activation of an Aptazyme effector; (2) in the identification, isolation and enhancement of allosteric effectors and of the allosterically regulatable aptazymes with which they interact; (3) to activate or repress a reporter gene (e.g. luciferase) containing an engineered intron in response to an endogenous activator; and (4) to monitor intracellular levels of proteins or small molecules such as cyclic AMP.
 XX

Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;
Best Local Similarity 100.0%; Pred. No. 5; 4e-38; Mismatches 0; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAGGTACTTATACGTGAACTCTAAACGGGAACTCTCTAGTAGA 60
1 GCCTGAGTATAGGTACTTATACGTGAACTCTAAACGGGAACTCTCTAGTAGA 60
DB 61 CAATCCCGTGCTTAATTATACCGATCCTTATGCCTTGCAGATAATGCCAAC 120
61 CAATCCCGTGCTTAATTATACCGATCCTTATGCCTTGCAGATAATGCCAAC 120
Db 61 CAATCCCGTGCTTAATTATACCGATCCTTATGCCTTGCAGATAATGCCAAC 120
61 CAATCCCGTGCTTAATTATACCGATCCTTATGCCTTGCAGATAATGCCAAC 120
QY 121 GACTATCCCT 131
121 GACTATCCCT 131
Db 121 GACTATCCCT 131

RESULT 4
ABNB3043
ID ABNB3033 standard; DNA; 131 BP.
XX
AC AAL43033;
XX
DT 25-SBP-2002 (first entry)
XX
DE Regulatable, catalytically active nucleic acid construction oligo #3.
XX
KW gene therapy; ds.
XX
OS Synthetic.

Key Location/Qualifiers
FH misc_feature 77 /*tag= a
FT /note= "represents between 1 and 4 unknown nucleotides"
FT 108 /*tag= b
FT /note= "represents between 1 and 4 unknown nucleotides"
XX
PN WO200196559-A2.
XX
PD 20-DEC-2001.
XX
FT 14-JUN-2001; 2001WO-US19302.
PR 15-JUN-2000; 2000US-212097P.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
PI Davidson E, Cox JC, Reidel T;
XX
DR WPI; 2002-090203/12.
XX
PT New regulatable, catalytically active nucleic acids (RCANA), useful in
gene therapy (particularly for regulating gene expression), or in
assays for detecting the presence of ligands or activation of an
effector of RCANA.
XX
Example 2; Page 42; 126pp; English.

The present invention relates to regulatable, catalytically active
nucleic acids (RCANAs) which are regulated by polypeptides. These are
useful for regulating gene expression, in assays for detecting the
presence of ligands, for activation of an effector of RCANA, and in gene
therapy. The present sequence is an oligonucleotide used in the
construction of an RCANA.

Sequence 131 BP; 37 A; 32 C; 24 G; 36 T; 2 other;

RESULT 5
ABNB3048
ID ABNB3048 standard; DNA; 131 BP.
XX
AC ABNB3048;
XX
DT 16-AUG-2002 (first entry)
XX
DE Aptazyme construct oligonucleotide GpIrhP6pool.
XX
KW Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; GpIrhP6pool; ss.
XX
OS Unidentified.
XX
FH misc_feature 77 /*tag= a
FT misc_feature 108 /*tag= a
FT /note= "Base may be repeated 1-4 times"
XX
PN WO200196541-A2.
XX
PD 20-DEC-2001.
XX
PR 15-JUN-2001; 2001WO-US19119.
XX
PR 15-JUN-2000; 2000US-0661658.
PA (TEXA) UNIV TEXAS.
XX
PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
PI Davidson E, Cox JC, Reidel T;
XX
DR WPI; 2002-090203/12.
XX
PT Aptazyme construct for detecting the presence of ligands, comprises a
regulatable Group I intron aptamer oligonucleotide with a regulatory
domain, and modulates their kinetic parameters in response to an
effector.
XX
PS Claim 10; Page 31; 42pp; English.
XX
The sequence represents an oligonucleotide used in the invention in the
construction of a group I regulatable aptazyme pool. The invention
relates to a novel aptazyme construct comprising a regulatable Group I
intron aptamer oligonucleotide sequence having an allosterically
regulatable regulatory domain, where the kinetic parameters of the
aptazyme on a target gene vary in response to the interaction of an
allosteric effector molecule with the regulatory domain, and the intron
splicing reaction occurs in vitro. The aptazyme is useful: (1) in assays
to detect the presence of ligands or to detect activation of an aptazyme
by an effector; (2) in the identification, isolation and enhancement of
allosteric effectors and of the allosterically regulatable aptazymes with
which they interact; (3) to activate or repress a reporter gene (e.g.

CC luciferase) containing an engineered intron in response to an endogenous activator; and (4) to monitor intracellular levels of proteins or small molecules such as cyclic AMP.

XX Sequence 131 BP; 37 A; 32 C; 24 G; 36 T; 2 other;

Matched 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCCTGAGTATAAGGTGACTATACGTGTTAATCTCTAAACGGGGAACTCTCTAGTACA 60

Db 1 GGCCTGAGTATAAGGTGACTATACGTGTTAATCTCTAAACGGGGAACTCTCTAGTACA 60

QY 61 CAATCCCGCTTAATTCAGCATGCTGCTGAGATAATGCCAAC 120

Db 61 CAATCCCGCTTAATTCAGCATGCTGCTGAGATAATGCCAAC 120

QY 119 AGCAGTATCCCT 131

Db 121 GACTATCCCT 131

Db 121 GACTATCCCT 131

RESULT 6

ID AAL43050 standard; DNA; 133 BP.

AC AAL43050;

XX

DT 25-SEP-2002 (first entry)

XX

DE Regulatable, catalytically active nucleic acid construction oligo #9.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

KW gene therapy; ds.

KW gene therapy; ds.

OS Synthetic.

PN WO200196559-A2.

XX

PD 20-DEC-2001.

XX

PP 14-JUN-2001; 2001WO-US19302.

XX

PR 15-JUN-2000; 2000US-212097P.

XX

PR (TEXA) UNIV TEXAS SYSTEM.

XX

PT Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

PI Davidson E, Cox JC, Reidel T;

XX

DR 2002-122216/16.

XX

WPI: 2002-122216/16.

XX

PT New regulatable, catalytically active nucleic acids (RCANA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA.

XX

PS Example 5; Page 68; 126pp; English.

XX

The present invention relates to regulatable, catalytically active nucleic acids (RCANAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the construction of an RCANA.

XX

Sequence 129 BP; 36 A; 32 C; 24 G; 37 T; 0 other;

Matched 129; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GGCCTGAGTATAAGGTGACTATACGTGTTAATCTCTAAACGGGGAACTCTCTAGTACA 60

Db 1 GGCCTGAGTATAAGGTGACTATACGTGTTAATCTCTAAACGGGGAACTCTCTAGTACA 60

QY 61 CAATCCCGCTTAATTCAGCATGCTGCTGAGATAATGCCAAC 120

Db 61 CAATCCCGCTTAATTCAGCATGCTGCTGAGATAATGCCAAC 120

Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 121 GACTATCCCT 131

|||||||

us-09-661-658B-2.Eng

PR 15-JUN-2000; 2000US-212097P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PT Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
 PI Davidson E, Cox JC, Reidel T;
 DR WPI; 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in assays for detecting the presence of ligands or activation of an effector of RCANA.

XX Example 5; Page 68; 126pp; English.

CC The present invention relates to regulatable, catalytically active nucleic acids (RCANAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene construction of an RCANA.

CC Sequence 115 BP; 30 A; 30 C; 22 G; 33 T; 0 other;

CC Best Local Similarity 91.9%; Pred. No. 1.2e-20; Length 115; Matches 102; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 GCCTAGATTAAGGTGACTTATGTTAACTCATTAACGGGAACTCTAGATA 60
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 GGCCTGAGTATAAGGTGACTTATGTTAACTCATTAACGGGAACTCTAGATA 60
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 CAATCCCGTGCTAAATTATCAGCATGTCCTGAGCCCTGGAGATA 111
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 CAATCCCG-----TATACCAGCATGTCCTGAGCCCTGGAGATA 103
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 11
 AAL43067
 ID AAL43067 standard; RNA; 82 BP.

AC AAL43067;

XX DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid #2.

XX KW Regulatable, catalytically active nucleic acid; RCANA; ribozyme;

KW gene therapy; ss. catalytically active nucleic acid #2.

OS Unidentified.

XX
 FH KEY misc_binding Location/Qualifiers
 FT misc_binding /tag= a
 FT stem_loop /bound_moiety= "binds nucleotides 33-29 of itself"
 FT misc_binding /tag= b
 FT misc_binding /tag= c
 FT misc_binding /bound_moiety= "binds nucleotides 8-4 of itself"
 FT misc_binding /tag= d
 FT misc_binding /bound_moiety= "binds nucleotides 79-78 of itself"
 FT misc_binding /tag= e
 FT misc_binding /bound_moiety= "binds nucleotide 72 of itself"
 FT misc_binding /tag= f
 FT stem_loop /bound_moiety= "binds nucleotides 68-67 of itself"
 FT stem_loop /*tag= g

FT misc_binding 67..68
 FT /*tag= h
 FT /bound_moiety= "binds nucleotides 46-45 of itself"
 FT misc_binding 72
 FT /*tag= i
 FT /bound_moiety= "binds nucleotide 41 of itself"
 PT misc_binding 78..79
 FT /*tag= j
 FT /bound_moiety= "binds nucleotides 35-34 of itself"
 PN WO200196559-A2.
 XX WO200196559-A2.
 PD 20-DEC-2001.

XX PF 14-JUN-2001; 2001WO-US19302.

XX PR 15-JUN-2000; 2000US-212097P.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
 DR WPI; 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in assays for detecting the presence of ligands or activation of an effector of RCANA.

XX Example 1; Fig 2A; 126pp; English.

CC The present invention relates to regulatable, catalytically active nucleic acids (RCANAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene exemplification of the invention.

XX Sequence 82 BP; 24 A; 21 C; 16 G; 21 U; 0 other;

CC Best Local Similarity 74.4%; Pred. No. 3.5e-20; Length 82; Matches 61; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

QY 37 TAAGGGGACCTCTAGTAGACAATCCGGCTAAATTACGAGCATCGTCCTGAT 96
 ||||||| ||||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 1 URAAGGGGACCCUCUGAGACAUCCGGUCAAUAUACCAGCAUGCUUGAU 60
 ||||||| ||||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 61 GCCCUUGGAGAUAAAUGCUA 82

RESULT 12
 AAL43090
 ID AAL43090 standard; RNA; 82 BP.

AC AAL43090;

XX DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid #22.

XX KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

KW gene therapy; ss.

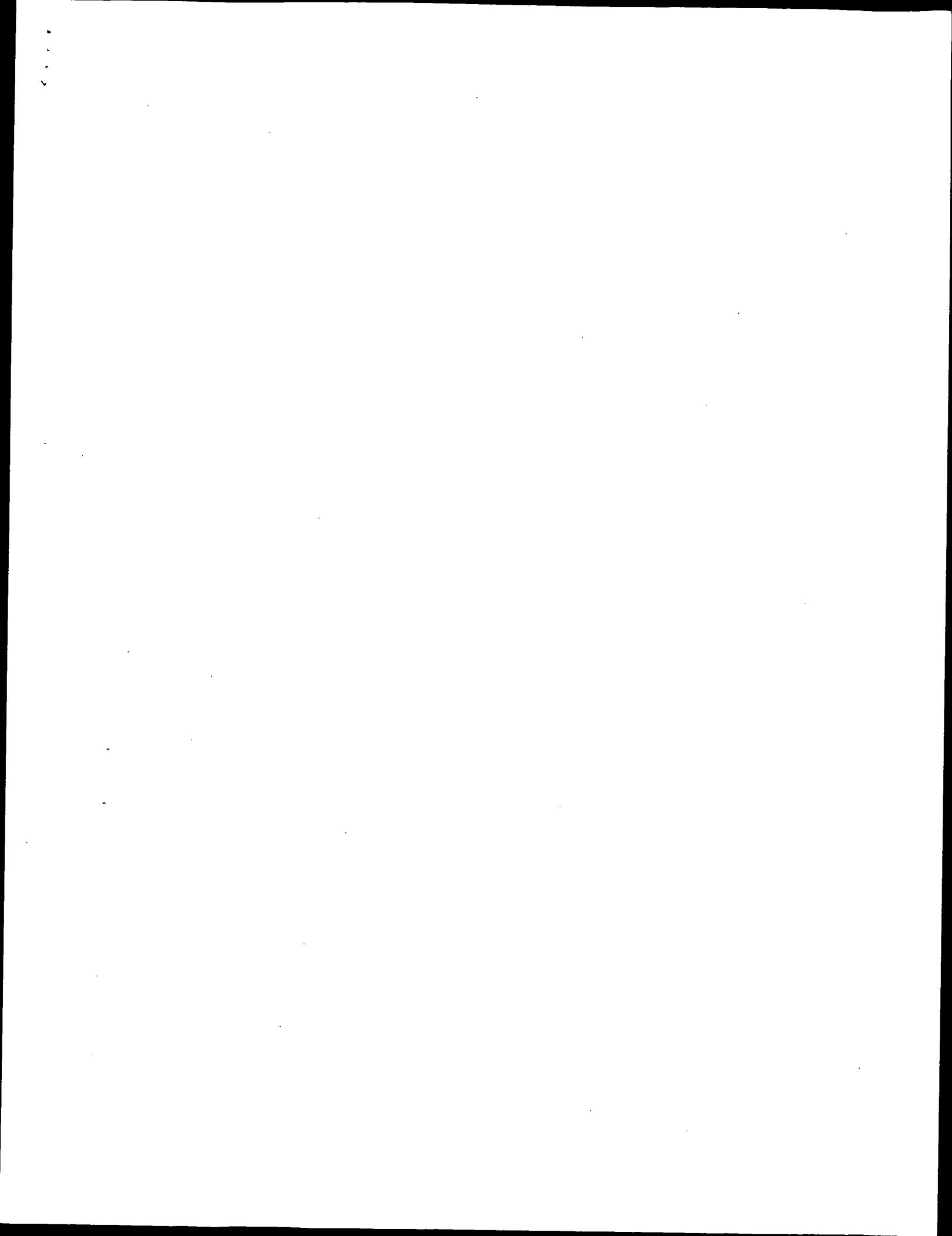
OS Unidentified.

XX
 FH KEY misc_binding Location/Qualifiers
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 FT misc_binding /*tag= a
 FT misc_binding /bound_moiety= "binds nucleotides 33-29 of itself"
 FT misc_binding /tag= b
 FT misc_binding /tag= c
 FT misc_binding /bound_moiety= "binds nucleotides 8-4 of itself"
 FT misc_binding /tag= d
 FT misc_binding /bound_moiety= "binds nucleotides 79-78 of itself"
 FT misc_binding /tag= e
 FT misc_binding /bound_moiety= "binds nucleotide 72 of itself"
 FT misc_binding /tag= f
 FT misc_binding /bound_moiety= "binds nucleotides 68-67 of itself"
 FT misc_binding /*tag= g

us-09-661-658b-2.rng

Tue Jul 15 10:33:02 2003

us-09-661-658b-2.rng



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GenCore Version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 13, 2003, 21:34:47 ; Search time 1135 Seconds
 (without alignments)
 1869,259 Million cell updates/sec

Title: US-09-661-658B-2
 Perfect score: 131
 Sequence: ggctgagataaagggtgactt.....atgccttaacgaccatccctt 131

Scoring table: IDENTITY NUC
 Gapop 10.0 , gapext: 1.0

Searched: 16154066 seqs, 8097743376 residues

total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database : EST:
 1: em_estba: *
 2: em_esthun: *
 3: em_estin: *
 4: em_estml: *
 5: em_estov: *
 6: em_estpi: *
 7: em_estro: *
 8: em_htc: *
 9: gb_est1: *
 10: gb_htc: *
 11: gb_est2: *
 12: gb_est3: *
 13: gb_est4: *
 14: gb_est5: *
 15: em_estrun: *
 16: em_estom: *
 17: gb_gss: *
 18: em_gss_hum: *
 19: em_gss_inv: *
 20: em_gss_p1n: *
 21: em_gss_vrt: *
 22: em_gss_fun: *
 23: em_gss_mam: *
 24: em_gss_mus: *
 25: em_gss_other: *
 26: em_gss_pro: *
 27: em_gss_rnd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	32.8	25.0	525	17	BH280107 CH330-117
2	31.6	24.1	443	10	AW989890 uff9h10.Y
3	31.6	24.1	1068	11	AK017255 Mus musculus
4	31.2	23.8	682	17	BH245494 PSB0764 S
5	31.1	23.7	570	17	A0060314 CIT-HSP-2
6	30.8	23.5	340	17	AZ489123 IM0319E4

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	BH280107	CH330-117E23. TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone	BH280107	1	GSS	30-NOV-2001	Rattus norvegicus
2	BH280107	CH330-117E23. DNA sequence.	BH280107	1	GII:17192509		
3	BH280107		BH280107.1	1	GI:17192509		
4	BH280107						
5	BH280107						
6	BH280107						
7	BH280107						
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24	BH280107						
25	BH280107						
26	BH280107						
27	BH280107						

REFERENCE

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebrge-Georgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.

TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment

JOURNAL Unpublished

COMMENT Contact: Shuying Zhao

Department of Eukaryotic Genomics
 The Institute for Genomic Research
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TeL: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Copies are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.html>). For BAC library

availability, please contact Pieter de Jong (pdejong@email.cho.org).

Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or_ering_information.htm). BAC end

page: http://www.tigr.org/tigrdb/bac_ends/rat/bac_end_intro.html

Plate: 117 row: E column: 23

Seq primer: sp6

Class: BAC ends.

Location/Qualifiers

1. .525

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/strain="BN/SNHSd/MCW"

/clone_id="CH230-117E23"

/clone_lib="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="Vector: PTARBA2.1; Site_1: EcoRI; Site_2: EcoRI;

CHORI-230 Rat (BN/SNHSd/MCW) BAC library produced by

Pieter de Jong"

BASE COUNT 165 a 88 c 86 g 186 t

ORIGIN

Query Match 25.0%; Score 32.8; DB 17; Length 525;

Best Local Similarity 59.8%; Pred. No. 1.7; Mismatches 0; Indels 37; Gaps 0; Gaps 0;

Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 TGTAGTATAGGAGTACTATCTGTAACTCTAACGGGAACCTCTCTAGTAGACAA 63

Db 44 TGCTGTGGGTGACTTTTTCATGATCTCTAATCATGAGATTCCATAGTAGTCAA 103

QY 64 TCCCGTGCTAAATTACCCACATGCTGCA 95

Db 104 TCTTGGAGCACACACTACAAGAATAGTGTATA 135

RESULT 2

AW989880/c

LOCUS AW989880

DEFINITION 443 bp mRNA

IMAGE:1511875 5', mRNA sequence..

ACCESSION AW989880

VERSION AW989880.1

KEYWORDS EST.

SOURCE

ORGANISM Mus musculus

DEFINITION

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1. (bases 1 to 443) NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strauberg, Ph.D.

Email: cgabbs.r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (<http://image.llnl.gov>) for further information.

MG:9:38727

Seq primer: 40RP from Gibco.

FEATURES location/Qualifiers

1. .443

/organism="Mus musculus"

/clone_id="IMAGE:1511875"

/clone_lib="Scares_mammary_gland_NMLMG"

/tissue_type="mammary_gland"

/lab_host="DH10B"

/note="Vector: pT7T3-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." BASE COUNT 125 a 95 c 115 g 108 t ORIGIN

Query Match 24.1%; Score 31.6; DB 10; Length 443;

Best Local Similarity 60.5%; Pred. No. 4; Mismatches 0; Indels 0; Gaps 0;

Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GCCTGAGATAAGGTGACTTACTCTGTAACCTATCTAACGGGAACCTCTCTAGTGA 60

Db 314 GCTTGAGSPACATCTGACATTCATCTAAGTCAGCAGACACAGAAAATCTCTCCAGCCGA 255

QY 61 CAATCCCTGCTAATATATACAGCA 86

Db 254 GACGCCGCGCTAGGGTACACTCGAA 229

RESULT 3

AK017255/c

LOCUS AK017255

DEFINITION 1068 bp mRNA

LINEAR

AK017255

Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched

sequence.

ACCESSION AK017255

VERSION 1 GI:12856401

KEYWORDs HTC; CAP trapper.

SOURCE Mus musculus (strain: C57BL/6J) 6 days neonate head cDNA to mRNA,

clone_lib: RIKEN full length enriched mouse cDNA library

clone_id: J0401H09.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CARNINI, P.

REFERENCE

1. CARNINI, P. and HAYASHIZAKI, Y.

TITLE High-efficiency full length cDNA cloning

JOURNAL Meth. Enzymol.

303, 19-44 (1999)

PUBMED 9927953

REFERENCE

2. CARNINI, P., SHIBATA, Y., HAYATSU, N., SUGAHARA, Y., SHIBATA, K., ITOH, M., KONNO, H., OKAZAKI, Y., MURAMATSU, M. and HAYASHIZAKI, Y.

TITLE Normalization and subtraction preparation full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res.

10 (10), 1617-1630 (2000)

PUBMED 11042159

REFERENCE

3. SHIBATA, K., ITOH, M., AIZAWA, K., NAGAOKA, S., SASAKI, N., CARNINI, P., KONNO, H., AKIYAMA, J., NISHI, K., KITSUNAI, T., TASHIRO, H., ITOH, M., SUMI, N., ISHLI, Y., NAKAMURA, S., HAZAMA, M., NISHINE, T., HARADA, A., YAMAMOTO, R., MATSUMOTO, H., SAKAGUCHI, S., IKEGAMI, T., KASHIWAGI, K., FUJIWARA, S., INOUE, K., TOGAWA, Y., IZAWA, M., OHARA, E., WATANAKI, M., YONEDA, Y., ISHIKAWA, T., OZAWA, K., TANAKA, T., MATSUURA, S., KAWAI, J., OKAZAKI, Y., MURAMATSU, M., INOUE, Y., KIRA, A. and HAYASHIZAKI, Y.

TITLE RIKEN integrated sequence analysis pipeline (RISA) system - 384 format

JOURNAL Genomic Res.

10 (11), 1757-1771 (2000)

PUBMED 1103913

REFERENCE

4. KAWAI, J., SHINAGAWA, A., SHIBATA, K., YOSHINO, M., ITOH, M., ISHLI, Y., CARNINI, P., HAGIWARA, T., HATA, A., FUKUNISHI, Y., KONNO, H., ADACHI, J., FUKUDA, S., SAITO, T., OHAZAKI, Y., GOROBORI, T., BONO, H., KASUKAWA, T., Saito, R., KODOMA, K., MATSUDA, H., ASHBURNER, M., BATALLON, S., CASAVANT, T., KUEHL, P., LEWIS, S., MATSUO, Y., NIKAIDO, I., PESOLE, G., KING, B., KOCHIWA, H., QUACKENBUSH, J., SCHIRMER, L.M., STABILIS, F., SUZUKI, R., TOMITA, M., WAGNER, L., WASHIO, T., SAKAI, K., OKIDO, T., FURUYA, M., AONO, H., BALDARELLI, R., BARSH, G., BLAKE, J., BOFFELLI, D., BOIJUNGA, N., CARNINI, P., DE BORALDO, M.F., BROWNSTEIN, M.J., BUIT, C., FLETCHER, C., FUJITA, M., GARIBOLDI, M., GUSTINCICH, S., HILL, D.,

us-09-661-658b-2.fst

	TITLE	Nature 409 (6821), 685-690 (2001)
JOURNAL	MEDLINE	21085660
PUBLMED	11217851	
REFERENCE	5 (bases 1 to 1058)	
AUTHORS	Adachi,J., Alzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bonc,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,M., Hiraoka,I., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,Y., Konno,H., Koya,S., Kuroki,Y., Kurihara,C., Matsuzawa,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Onno,M., Okazaki,Y., Okido,T., Owa,C.C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibaoka,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagami,M., Takanashi,F., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	
TITLE	JOURNAL	Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp; URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT		Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
		CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer adapter of sequence [5'-GAGAGAGAGAGATCAGACGGCTTGTTCATTGTTNN3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAAGAGAGAGATCTGGTAATTAAATCCCGCCCCCCC 3']. cDNA was cleaved with BamHI and XbaI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
FEATURES	source	Location/Qualifiers
		1. . 1068 /organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="FANTOM_DB:5430401H09"
		/db_xref="MGD:MG:1903925"
		/db_xref="taxon:10090"
		/clone="5430401H09"
		/tissue,type="head"
		/clone_id="RIKEN full-length enriched mouse cDNA library"
		/dev_stage="6 days neonate"
		1. . 1068 /note="evidence:NAS hypothetical protein"
		/db_xref="MGD:MG:191846"
BASE COUNT	308 a	210 c 218 g 332 t
ORIGIN		
Query Match	24.1%	Score 31.6; DB 11; Length 1068;
Best Local Similarity	60.5%	Pred. No. 6; Mismatches 0;
Matches	52;	Conservative 0; Gaps 0;
misc_feature		
RESULT	5	
Q0060314		
LOCUS	A0060314	
DEFINITION	CIT-HSP-235103.TR CIT-HSP Homo sapiens genomic clone 235103, DNA sequence.	
QY	61	CAATCCGGTGTAAATTATACAGCA 86
Db	152	GACCGCGCTGCTAGGGTACACTCGA 127
RESULT	4	
BH245494/c		
LOCUS	BH245494	
DEFINITION	S. bicolor BTx623 PstI-digested total genomic DNA	
ACCESSION	PSB0764	
VERSION	BH245494.1	
KEYWORDS	GSS.	
SOURCE	sorghum.	
ORGANISM	Sorghum bicolor	
REFERENCE	Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC-clade; Panicoideae; Andropogoneae; Sorghum.	
AUTHORS	(1 bases 1 to 682)	
TITLE	Characterization of RFLP clone sequences for gene discovery and SSR development in Sorghum bicolor (L.) Moench	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Patterson AH	
Plant Genome Mapping Laboratory		
University of Georgia Center for Applied Genetic Technologies		
Riverbend Research Laboratory, Room 162, 110 Riverbend Road, Athens		
GA 30602 USA		
Tel: 7065830162		
Fax: 7065830160		
Email: paterson@uga.edu		
Contig9; Linkage group I; similar to EST BE366001		
Insert Length: 682		
Seq Primer: M13F/M13R		
Class: RFLP probe.		
FEATURES	source	Location/Qualifiers
		1. . 602 /organism="Sorghum bicolor"
		/cultivar="BTx623"
		/ab_xref="Taxon:4558"
		/clone="PS0764"
		/clone_id="S. bicolor BTx623 PstI-digested total genomic DNA library"
		/tissue-type="Leaf"
		/dev-stage="Immature"
		/note="vector: pMT7/T3; Site_1: PstI; Sorghum bicolor (L.) Moench"
BASE COUNT	216 a	168 c 107 g 191 t
ORIGIN		
Query Match	23.8%	Score 31.2; DB 17; Length 682;
Best Local Similarity	56.6%; Pred. No. 6; Mismatches 48; Indels 0; Gaps 0;	
Matches	60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;	
QY	7	GTATAAGTGACTATAGTGATCTATCTAACGAGGAACCTCTCTAGTAGACATCC 66
Db	368	GTATAAGTGAGGAACCTCTATATATACCTATATAAACCTCTGCTGTAGCAAG 309
QY	67	CGTCTAAATTATACAGCATGCTGTATGCCCTGGCAGATAATG 114
Db	308	CAAGCCAAATTATACAGCACTGTGAGGTGCAAGTGTAGGTTAAGG 261

ACCESSION A0060314
 VERSION AQ060314.1
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 510)
 AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, P., Suh, E., Wible, C., Shizuya, H., Simon, M., and Venter, J.C.,
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
 COMMENT Unpublished (1998)
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@igr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
[http://www.tigr.org/tgb/hungen/bac_end_search.html](http://www.tigr.org/tgb/hungen/bac_end_search/bac_end_search.html).
 Seq primer: M13 Reverse Class: BAC ends.
 FEATURES location/Qualifiers
 source 1. .570/
 /organism="Homo sapiens"
 /db_xref=taxon:9606"
 /clone="335103"
 /clone_lib="CIT HSP"
 /sex="Male"
 /cell_type="sperm"
 /note="vector: pBelOBAC11; Site_1: HindIII; Site_2: HindII"
 BASE COUNT 122 a 101 c 120 g 227 t
 ORIGIN
 Query Match 23.7%; Score 31; DB 17; Length 570;
 Best Local Similarity 62.0%; Pred. No. 7.1; Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Qy 10 TAAGCTGATTAATCTGAACTCTAAGGGGAACTCTCTAGTAGACAATCCGT 69
 Db 375 TCACTGTTATTGCTTAACTGTTATGCTGTATACATTATGACTTGATAT 434
 Qy 70 GCTAAATATACCGACATC 88
 Db 435 GTAAACATPACCTGCATC 453
 RESULT 6 AZ489123
 LOCUS A489123
 DEFINITION 340 bp linear GSS 05-OCT-2000
 ACCESSION A489123
 VERSION 1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 340)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenin, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R., plasmid inserts. Title: Mouse whole genome scaffolding with paired end reads from 10kb unpublished (2000) Contact: Robert B. Weiss
 JOURNAL COMMENT
 REFERENCE 1 (bases 1 to 1004)
 AUTHORS Roest-Crollius, H., Jaijou, O., Basilia, C., Bouneau, L., Fisher, C.,

ACCESSION A0060314
 VERSION AQ060314.1
 KEYWORDS GSS.
 SOURCE University of Utah Genome Center
 University of Utah
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn-genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0319 row: E column: 14
 Seq primer: CACAGGAAACACTATGACC
 Class: Plasmid ends
 High quality sequence stop: 340.
 FEATURES location/Qualifiers
 source 1. .340/
 /strain="Mus musculus"
 /db_xref="taxon:10000"
 /clone="UUCICM0319E14"
 /sex="Male"
 /lab_host="E. coli strain X110-gold, T1-resistant, F-"
 /note="Vector: pWD221; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www-jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of pRSI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptored vector DNA, and transformed into ampicillin resistance." Stratagene cells and selected for ampicillin resistance.

BASE COUNT 105 a 66 c 34 g 135 t
 ORIGIN
 Query Match 23.5%; Score 30.8; DB 17; Length 340;
 Best Local Similarity 58.9%; Pred. No. 6.5; Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 Qy 21 ATACTGATCATCAAAGGGGACCTCTAGTACAAATCCGGCTAAATA 80
 Db 165 ATATCTTAACTATCAAAATGTTACCATTCAGAAAGCTGCCCTTCCATGAATC 224
 Qy 81 CCAGCATCTGTGATGCCCTGGAGATA 110
 Db 225 CAACTCTGTTGTTTACCTCTGAGAA 254
 RESULT 7 CNS049YL
 LOCUS CNS049YL
 DEFINITION Tetradaon nigroviridis 1004 bp linear GSS 21-MAY-2000
 ACCESSION AL281190
 VERSION AL281190.1
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostomi; Neoteleostei; Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontidae; Tetradontidae.
 REFERENCE 1 (bases 1 to 1004)
 AUTHORS Roest-Crollius, H., Jaijou, O., Basilia, C., Bouneau, L., Fisher, C.,

Tue Jul 13 10:33:00 -

TITLE	Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
JOURNAL	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 1004), Roest-Crollius,H., Dajillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1004)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cnrs.fr/~tetraodon .
FEATURES	Location/Qualifiers
Source	1..1004 /organism="Tetraodon nigroviridis" /db_xref="txon:99883" /clone="094B11" /clone_1_id="G" /clone_2_id="G" /feature="genoscope sequence" id="C0BG094CA05LP1-end" length="1004" type="DNA" version="25-JAN-2001"/>
BASE COUNT	248 a 257 c 261 g 224 t 14 others
ORIGIN	Query Match 23.4%; Score 30/6; DB 17; Length 1004;
	Best Local Similarity 54.0%; Pred. No. 13; Mismatches 51; Indels 0; Gaps 0;
Matches	61; Conservative 1; Mismatches 51; Indels 0; Gaps 0;
QY	2 CCTGGGTATAGGGACTATACCTGTAATCTAAACGGGAACCTCTAGTAGAC 61
Db	826 CCTAAATATAATDATCCATCTATCTATCTACTTTAATGTTAGGTACCCACCGATAGGCC 885
QY	62 AATCCGGTGTAAATTATACCAAGCACTCTGAGGCCCTGGAGATAATG 114
Db	886 TAGCCACAGCAGTATATCTAGCTTGCTGCCTCTCACCGATCAAGATG 938
RESULT	8
AZ742331	AZ742331 584 bp DNA linear GSS 25-JAN-2001
LOCUS	AZ742331.TV RPCI-24
DEFINITION	MUS musculus genomic clone RPCI-24-62F21, DNA sequence.
ACCESSION	AZ742331
VERSION	AZ742331.1 GI:12521098
KEYWORDS	house mouse, GSS.
ORGANISM	Mus musculus; Mus musculus; Euteleostomi; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Scurognathii; Muridae; Muridae; Mus. Mammalia; Ruthenia; Rodentia; Scurognathii; Muridae; Mus. 1 (bases 1 to 584)
REFERENCE	1 (bases 1 to 584) Zhao,S., Nieman,W., Malek,J., Shatsman,S., Aknret,B., Levins,M., Tsedaye,G., Geer,K., Krolik,M., Shvartzebein,A., Gebregeorgis,E., Russell,D., de Jong,P., and Fraser,C.M.
AUTHORS	Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other GSS: RPCI-24-62F21 TJ Contact: Shaying Zhao
TITLE	Department of Eukaryotic Genomics
JOURNAL	The Institute for Genomic Research
COMMENT	The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdj@jmg@mail.chio.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/Bacpac/orderingframe.htm). BAC end

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=784 Col=6 Row=K"
 /sex="male"
 /note="vector: PBACE2.6; Site_1: EcoRI; Site_2: EcoRI;
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 PBACE2.6 vector at EcoRI sites." DNA was cloned into the
 BASE COUNT 165 a 129 c 105 g 185 t 17 others
 ORIGIN

Query Match Best Local Similarity 22.6%; Score 29.6; DB 17; Length 601;
 Matches 50; Conservative 0; Mismatches 0; Gaps 0;
 QY 15 TGA
 Db 260 TA
 QY 75 ATTATC
 Db 320 AATAGA
 RESULT 10
 AQ239325 LOCUS L26622_c
 DEFINITION mRNA sequence.
 ACCESSION L26622.1
 VERSION GI:3671616
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM MUS musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 492)
 AUTHORS Kerr,S.M., Vambrie,S., McKay,S.J. and Cooke,H.J.
 TITLE Analysis of cDNA sequences from mouse testis
 JOURNAL Mamm. Genome 5, 557-565 (1994)
 COMMENT 95093181 Contact: Kerr,S.M., Vambrie,S., McKay,S.J. and Cooke,H.J.
 FEATURES Location/Qualifiers 1..492
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="B03"
 /note="vector: lambda unizip male testis"
 BASE COUNT 181 a 87 c 69 g 150 t 5 others
 ORIGIN
 Query Match Best Local Similarity 22.4%; Score 29.4; DB 14; Length 492;
 Matches 48; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 34 ATCA
 Db 79 ATCGA
 QY 94 GATGCC
 Db 19 ATTC
 RESULT 12
 AQ28517_c LOCUS AQ28517
 DEFINITION CITIB-EL-2653G12.TP CITIB-EL Homo sapiens linear GSS 16-JUN-1999
 ACCESSION Ad28517
 VERSION AQ28517.1
 KEYWORDS GSS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building

FEATURES source
 1..268
 /organism="Homo sapiens"
 /db_xref="GDB:7525738"
 /db_xref="taxon:9606"
 /clone="RPCI-11-68A11"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="vector: PBACE2.6; Site_1: EcoRI; Site_2: EcoRI;
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 PBACE2.6 vector at EcoRI sites." DNA was cloned into the
 BASE COUNT 92 a 37 c 41 g 97 t 1 others
 ORIGIN

JOURNAL		COMMENT	
Unpublished (1997)	Contact: Shaying Zhao, William Nierman, Mark Adams		
Department of Eukaryotic Genomics			
The Institute for Genomic Research			
9712 Medical Center Dr., Rockville, MD 20850			
Tel: 301 838 0200			
Fax: 301 838 0208			
Email: hbe@tigr.org			
Clones are available from Research Genetics (info@resgen.com). BAC			
end search page:			
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html .			
Seq primer: M13-21			
Class: BAC ends.			
FEATURES	Location/Qualifiers		
SOURCE	1. . 565		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="2053G12"		
	/clone_1_id="CIRBI-EL"		
	/sex="male"		
	/cell_type="sperm"		
	/note="Vector: pBelBAC11; Site_1: EcoRI; Site_2: EcoRI;		
	caltech Human BAC Library D"		
BASE COUNT	232 a 129 c 84 g 120 t		
ORIGIN			
RESULT 13			
Query Match	22.4%	Score 29.4	DB 17
Best Local Similarity	60.8%	Pred. No. 25	Length 565
Matches	48	Conservative	
	0	Mismatches	
		Indels	0
		Gaps	0
DEFINITION	D63293/c LOCUS		
	371 bp mRNA		
	linearity EST 29-AUG-1995		
ACCESSION	D63293		
VERSION	D63293.1		
KEYWORDS	EST		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE	1 (bases 1 to 371)		
AUTHORS	Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimaeda,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Makikawa,H., Shin,S., and Nakamura,Y.		
JOURNAL	Fujiwara et al. (1995)		
COMMENT	Unpublished (1995)		
CONTACT	Tsutomu Fujiwara		
OTSUWA GEN RESEARCH INSTITUTE	Otsuka Pharmaceutical Co.,Ltd		
	463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan		
	Tel: 0886-65-2888		
	Fax: 0886-37-1035.		
FEATURES	Location/Qualifiers		
SOURCE	1. . 371		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="GEN-519C10"		
	/clone_1_id="Clontech human placenta polyA+ mRNA (#6572)"		
BASE COUNT	128 a 51 c 51 g 141 t		
ORIGIN			
RESULT 14			
Query Match	22.3%	Score 29.2	DB 14
Best Local Similarity	62.2%	Pred. No. 24	Length 371
Matches	46	Conservative	
	0	Mismatches	
		Indels	0
		Gaps	0
DEFINITION	BQ634483 LOCUS		
	414 bp mRNA		
	linearity EST 03-JUL-2002		
ACCESSION	BQ634483		
VERSION	BQ634483.1		
KEYWORDS	EST		
SOURCE	Pinus taeda		
ORGANISM	Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.		
REFERENCE	1 ((bases 1 to 414))		
AUTHORS	Sederoff,R.		
TITLE	Molecular Basis of Wood Formation in the Pine Megagenome		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Johnson, Arthur		
	North Carolina State University		
	Tel: 919 515 7800		
	Fax: 919 515 7801		
	Email: ajohnson@unity.ncsu.edu		
FEATURES	Location/Qualifiers		
SOURCE	1. . 414		
	/organism="Pinus taeda"		
	/strain="Coastal plain loblolly pine from North Carolina"		
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	/clone="NXRV069_E06_5"		
	/clone_1_id="NXRV (NSF Xylem Root wood vertical)"		
	/tissue_type="Xylem"		
	/cell_type="Root (primary)"		
	/dev_stage="transitional"		
	/lab_host="XIL-Blue"		
	/note="Vector: pBluescript SK-; Site_1: Eco RI; Site_2: Xba I; The library is from primary xylem scraped from the roots of a twelve year old tree in the transitional phase from juvenile wood to mature wood production. NOTE: The sequences contain a 'CONA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'ATTCGGACGAG'."		
BASE COUNT	158 a 61 c 68 g 114 t 13 others		
ORIGIN			
RESULT 15			
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Best Local Similarity	54.1%	Pred. No. 29	Length 414
Matches	59	Conservative	
	0	Mismatches	
		Indels	0
		Gaps	0
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	linearity GSS 29-AUG-20000		

DEFINITION SP_0062_B1_B11_T7A Strongylocentrotus purpuratus, purple sea urchin , sperm genomic BAC library Strongylocentrotus purpuratus genomic
 ACCESSION AZ159311
 VERSION AZ159311.1
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus.
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 REFERENCE 1 (bases 1 to 545)
 AUTHORS Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
 Swartzell,S., Wallace,J.C., Postka,A.J., Livingston,B.T., Wray,
 G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and
 Hood,L.
 TITLE A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 MEDLINE 2002566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-6421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 62 row: D column: 21
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 545.
 FEATURES location/qualifiers
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 /clone_id="Strongylocentrotus purpuratus, purple sea
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 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli
 DH10B"
 BASE COUNT 151 a 86 c 116 g 177 t 15 others
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 Best Local Similarity 58.8%; Pred. No. 33;
 Matches 50; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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 Db 453 TGAAGTTATGGGAGAATTTTTAATATATCAGACTGGACCTCTAGGCAGA 512
 Oy 64 TCCCGTGCTAAATTATACAGCATC 88
 Db 513 TCCCATCTCATTTCTAGCTTC 537

Search completed: July 13, 2003, 22:35:19
 Job time : 1140 secs

us-09-661-658b-2.rni

Tue Jul 15 10:33:02 2003
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nucleic search, using SW model
July 13, 2003, 19:59:57 ; search time 37 seconds
(without time alignments) cell updates/sec
Run on:
US-09-661-658B-2
atgcataacgactatccctt 131

C	44	US-08-223-305C-29
C	43	US-09-3614-34-6
C	42	US-09-6355-025-10
C	41	US-09-6355-025-10
C	40	US-09-3614-34-6
C	39	US-09-3614-34-10
C	38	US-09-3614-34-10
C	37	US-08-984-272-3
C	36	US-08-984-272-3
C	35	US-08-984-272-3
C	34	US-08-984-272-3
C	33	US-08-984-272-3
C	32	US-08-450-562-3
C	31	US-08-450-562-3
C	30	US-08-194-986-3
C	29	US-08-194-986-3
C	28	US-08-193-05C-3
C	27	US-08-223-305C-3
C	26	US-08-455-542A-3
C	25	US-08-455-542A-3
C	24	US-08-455-542A-3
C	23	US-08-455-542A-3
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C	0	US-08-455-542A-3

Scoring table:				
441362 seqs.	15339381 residues			
searched:	892724			
total number of hits satisfying chosen parameters:	1			
Database :	Maximum DB seq length: 0 Minimum DB seq length: 200000000 Post-processing: Maximum Match 100% Listing first 45 summaries			
Issued_patents_NA:*	Match 0%			
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2: /cgn2_6/podata/1/ina/6A_COMB.seq:*	and is derived by analysis of the total score distribution.			
3: /cgn2_6/podata/1/ina/pcrus.Comb.seq:*	pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the total score distribution.			
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2	37.2	28.4	1 US-09-257-503A-24	FILING DATE: 01-MAY-1995
3	37.2	28.4	1 US-09-257-503A-28	CLASSIFICATION DATA: 435
4	37.2	28.4	1 US-05-09-257-503A-29	PATENT NUMBER: 02307E-070000US
5	37.2	28.4	1 US-08-443-957-37	PRIORITY NUMBER: 19-MAY-1993
6	37.2	28.4	1 US-08-443-957-37	REGISTRATION NUMBER: 02307E-070000US
7	31.8	23.2	1 US-08-443-957-6	REFERENCE/DOCKET NUMBER: 02307E-070000US
8	30.4	23.2	1 US-08-852-852-20	TELECOMMUNICATION INFORMATION: (415) 576-0300
9	28.4	21.7	1 US-09-052-558-1	TELEPHONE: (415) 576-0300
10	28.4	21.7	1 US-08-887-254-01	TELEFAX: (415) 576-0300
11	28.4	21.7	1 US-09-109-207C-1	ID: 1:
12	28.4	21.7	1 US-09-296-0015-9	INFORMATION FOR SEQ ID: 1:
13	28.4	21.7	1 US-09-493-838-5	SEQUENCE LENGTH: 510 base Pairs
14	27.4	20.9	1 US-08-493-838-5	TYPE: nucleic acid
15	27.4	19.8	1 US-09-503A-33	STRANDEDNESS: single
16	26	19.2	1 US-07-891-9426-4	TOPOLOGY: linear
17	25.2	19.2	1 US-07-891-9426-7	MOLECULE TYPE: RNA
18	25.2	19.2	1 US-09-356-952-12	SEQUENCE ID: 1:
19	25.2	19.2	1 US-09-356-075-1	APPLICANT: Ford, Ethan E.
20	25.2	18.9	1 US-09-221-017B-19	APPLICANT INVENTION: RNA Cyclase Ribozymes
21	24.6	18.8	1 US-08-487-826B-11	ATTORNEY/AGENT: Ares, Manuel E.
22	24.6	18.8	1 US-08-487-826B-11	CITY: San Francisco
23	24.6	18.8	1 US-09-210-288-11	STATE: California
24	24.6	18.8	1 US-08-487-826B-13	COUNTRY: USA
25	24.6	18.8	1 US-08-455-543A-29	ZIP: 94111-3834
26	24.6	18.8	1 US-08-455-543A-29	FILED DATE: 01-MAY-1995
27	18.6	17.9	1 US-08-431-8968-1	CLASSIFICATION DATA: 435
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us-09-661-658b-2.rni

Db 341 GCCUGAGUAAAUGUGACAUAAUCUGUAACUAAUCUAACGGGAACCUUCUAGUAGA 400
 Qy 61 CAATCCGCGCTTAATATA 80
 Db 401 CAUCCGGUGCUAAUUGUA 420

RESULT 2

US-09-257-503A-30

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; Patient No. 6387617

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION:

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER:

; PRIOR FILING DATE:

; PCT/IL97/00282

; PRIOR FILING DATE:

; 1996-08-26

; PRIOR APPLICATION NUMBER:

; 1996-08-26

; NUMBER OF SEQ ID NOS:

; 1997-03-17

; SEQ ID NO:

; LENGTH:

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; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-30

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Best Local Similarity

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Length 59;

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; Conservative

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; Pred. No. 4.5e-05;

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; Indels 8;

; Gaps 0;

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; TYPE: RNA

; ORGANISM: Humanus

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Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 33;

; Conservative

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; Gaps 0;

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; LENGTH:

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; TYPE: RNA

; ORGANISM: Humanus

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Query Match

Best Local Similarity

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Length 123;

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78

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; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-30

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-30

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-30

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-30

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-30

Query Match

Best Local Similarity

28.4%

Score 37.2; DB 4; Length 149; ; Matches 29; ; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA 78; ; SEQ ID NO: 28; ; LENGTH: 149; ; TYPE: RNA; ; ORGANISM: Humanus; ; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

; SEQ ID NO:

; LENGTH:

; 149

; TYPE: RNA

; ORGANISM: Humanus

; US-09-257-503A-28

Query Match

Best Local Similarity

28.4%

Score 37.2;

DB 4;

Length 149;

; Matches 29;

; AACCTATCAAACGGGAACCTCTCTAGAGACAACTCCGNGCTAAATTA

78

RESULT 6
US-08-443-957-29
; Sequence 29, Application US/08443957
; Patent No. 5580737

GENERAL INFORMATION:
APPLICANT: Barry Polisky
APPLICANT: Robert Jenison
APPLICANT: Larry Gold
TITLE OF INVENTION: HIGH-AFFINITY NUCLEIC ACID LIGANDS THAT DISCRIMINATE BETWEEN THEOPHYLLINE AND CAFFEINE
TITLE OF INVENTION: CAFFEINE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 800 Kb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443, 957
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/134, 028
FILING DATE: 10-OCTOBER 1993
ATTORNEY/APPLICATION NUMBER: US/08/443, 957
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/536, 428
FILING DATE: 11-JUNE 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NX11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOGY: linear
US-08-443-957-29

RESULT 7
US-08-443-957-37
; Sequence 37, Application US/08443957
; Patent No. 5580737

GENERAL INFORMATION:
APPLICANT: Barry Polisky
APPLICANT: Robert Jenison
APPLICANT: Larry Gold
TITLE OF INVENTION: HIGH-AFFINITY NUCLEIC ACID LIGANDS THAT DISCRIMINATE BETWEEN THEOPHYLLINE AND CAFFEINE
TITLE OF INVENTION: CAFFEINE
TITLE OF INVENTION: CAFFEINE
NUMBER OF SEQUENCES: 37

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 800 Kb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443, 957
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/134, 028
FILING DATE: 10-OCTOBER 1993
APPLICATION NUMBER: 07/714, 131
FILING DATE: 10-JUNE 1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/536, 428
FILING DATE: 11-JUNE 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NX11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOGY: linear
US-08-443-957-37

RESULT 8
US-08-443-957-6
; Sequence 6, Application US/08443957
; Patent No. 5580737

GENERAL INFORMATION:
APPLICANT: Barry Polisky
APPLICANT: Robert Jenison
APPLICANT: Larry Gold
TITLE OF INVENTION: HIGH-AFFINITY NUCLEIC ACID LIGANDS THAT DISCRIMINATE BETWEEN THEOPHYLLINE AND CAFFEINE
TITLE OF INVENTION: CAFFEINE
TITLE OF INVENTION: CAFFEINE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 800 Kb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443, 957
 FILING DATE: ;
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/134, 028
 FILING DATE: 10 OCTOBER 1993
 APPLICATION NUMBER: 07/714, 131
 FILING DATE: 10-JUNE-1991
 APPLICATION NUMBER: 07/536, 428
 FILING DATE: 11-JUNE-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33-215
 REFERENCE/DOCKET NUMBER: NEX11
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 S-08-443-957-6

RESULT 9
 Sequence Match 23.2%; Score 30.4; DB 1; Length 40;
 Best Local Similarity 68.8%; Pred. No. 0.013; Mismatches 9; Indels 1; Gaps 0;
 Matches 22; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Query Match 21.7%; Score 28.4; DB 3; Length 5140;
 Best Local Similarity 53.6%; Pred. No. 0.55; Mismatches 59; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 TATAGGGACTTATCTGATCTAACGGGAACCTCTAGACATCCC 67
 Db 2436 TTATACAAAATTAAACGGAAATTAACTTAACGGATTCATAATTCCGATCC 2377
 QY 68 GRCGTTAATTATACACCATGCTGTGATGCCCTTGCGAGATAATAGCCT 117
 Db 2376 GCGGTTAAAGCTCATCAGCGTGTGTCGAGCGATTCACAGRTGTTGCC 2327

RESULT 10
 Sequence 20, Application US/08825852
 Patent No. 6121416
 GENERAL INFORMATION:
 APPLICANT: Clark, Ross G.
 APPLICANT: Lowman, Henry B.
 APPLICANT: Robinson, Iain C.A.F.
 TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
 NUMBER OF SEQUENCES: 79
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 COMPUTER TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443, 957-8
 FILING DATE: 31-Mar-1998
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28, 616
 REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1896
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5140 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-09-052-888-20

RESULT 11
 Sequence 11, Application US-08-887-3529B-1/C
 Query Match 21.7%; Score 28.4; DB 4; Length 5140;
 Best Local Similarity 53.6%; Pred. No. 0.55; Mismatches 59; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 TATAGGGACTTATCTGATCTAACGGGAACCTCTAGACATCCC 67
 Db 2436 TTATACAAAATTAAACGGAAATTAACTTAACGGATTCATAATTCCGATCC 2377
 QY 68 GRCGTTAATTATACACCATGCTGTGATGCCCTTGCGAGATAATAGCCT 117
 Db 2376 GCGGTTAAAGCTCATCAGCGTGTGTCGAGCGATTCACAGRTGTTGCC 2327

Patent No. 5994511
 GENERAL INFORMATION:
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinBattin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/887,352B
 FILING DATE: 03 JUL 1997
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P1123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-1489

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 6127 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Circular
 ; US-08-887-352B-1

RESULT 12
 Query Match 21.7%; Score 28.4; DB 2; Length 6127;
 Best Local Similarity 53.6%; Pred. No. 0.59; Matches 59; Conservatve 0; Mismatches 51; Indels 0; Gaps 0;
 ; Sequence 1, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 CURRENT APPLICATION NUMBER: US/09/296,005
 CURRENT FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 08/887,352
 EARLIER FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 26
 SEQ ID NO 1
 LENGTH: 6127
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 NAME/KEY: Artificial Sequence
 LOCATION: 1-6127
 OTHER INFORMATION: Expression plasmid
 ; US-09-296-005-1

Query Match 21.7%; Score 28.4; DB 4; Length 6127;
 Best Local Similarity 53.6%; Pred. No. 0.59; Matches 59; Conservatve 0; Mismatches 51; Indels 0; Gaps 0;
 ; Sequence 1, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 CURRENT APPLICATION NUMBER: US/09/296,005
 CURRENT FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 08/887,352
 EARLIER FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 26
 SEQ ID NO 1
 LENGTH: 6127
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 NAME/KEY: Artificial Sequence
 LOCATION: 1-6127
 OTHER INFORMATION: Expression plasmid
 ; US-09-296-005-1

RESULT 13
 Query Match 21.7%; Score 28.4; DB 4; Length 6127;
 Best Local Similarity 53.6%; Pred. No. 0.59; Matches 59; Conservatve 0; Mismatches 51; Indels 0; Gaps 0;
 ; Sequence 1, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 CURRENT APPLICATION NUMBER: US/09/296,005
 CURRENT FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 08/887,352
 EARLIER FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 26
 SEQ ID NO 1
 LENGTH: 6127
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 NAME/KEY: Artificial Sequence
 LOCATION: 1-6127
 OTHER INFORMATION: Expression plasmid
 ; US-09-296-005-1

Query Match 21.7%; Score 28.4; DB 4; Length 6127;
 Best Local Similarity 53.6%; Pred. No. 0.59; Matches 59; Conservatve 0; Mismatches 51; Indels 0; Gaps 0;
 ; Sequence 1, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 CURRENT APPLICATION NUMBER: US/09/296,005
 CURRENT FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 08/887,352
 EARLIER FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 26
 SEQ ID NO 1
 LENGTH: 6127
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 NAME/KEY: Artificial Sequence
 LOCATION: 1-6127
 OTHER INFORMATION: Expression plasmid
 ; US-09-296-005-1

RESULT 14
 US-08-468-819-89/c
 ; Sequence 89, Application US/08468819
 ; Patent No. 5871723
 ; GENERAL INFORMATION:
 APPLICANT: Strieter, Robert M.
 APPLICANT: Polverini, Peter J.
 APPLICANT: Kunkel, Steven L.
 TITLE OF INVENTION: CXC Chemokines as Regulators of Angiogenesis
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: US
 ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

<p>nts nucleic Acids</p> <p>gth 131: dels 0; gaps 0;</p> <p>GGAACTCTCTAGTAGA 60 GGAACTCTCTAGTAGA 60</p> <p>GCAAGATAATGCCCTAAC 120 GCAGATAATGCCCTAAC 120</p>	<p>Sequence 62, Appl Sequence 62, Appl Sequence 61, Appl Sequence 61, Appl Sequence 174, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 99, Appl Sequence 1, Appl Sequence 36, Appl Sequence 89, Appl Sequence 165, Appl Sequence 374, Appl Sequence 412, Appl Sequence 250, Appl Sequence 282, Appl Sequence 2610, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2687, Appl Sequence 7468, Appl Sequence 1075, Appl</p>
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Publication No. US20030104520A1
GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

CURRENT APPLICATION NUMBER: US/09/883, 119A

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGTH: 131

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: oligonucleotide

US-09-883-119A-20

Query Match 100.0%; Score 131; DB 9; Length 131;

Best Local Similarity 100.0%; Pred. No. 1.8e-37;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAAACGGGAACCTCTTAGTGA 60

Db 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAAACGGGAACCTCTTAGTGA 60

QY 61 CAATCCGGTGAATATTACCGATCGCTGATGCCCTGGAGNTAAATGCCAAC 120

Db 61 CAATCCGGTGAATATTACCGATCGCTGATGCCCTGGAGNTAAATGCCAAC 120

QY 121 GACTATCCCT 131

Db 121 GACTATCCCT 131

RESULT 3
US-09-883-119A-5

Sequence 5 Application US/09/883/119A

Publication No. US20030104520A1
GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents

TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050

CURRENT APPLICATION NUMBER: US/09/883, 119A

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 133

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: oligonucleotide

US-09-883-119A-21

Query Match 98.2%; Score 109; DB 9; Length 133;

Best Local Similarity 98.5%; Pred. No. 1.5e-29;

Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAAACGGGAACCTCTTAGTGA 60

Db 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAAACGGGAACCTCTTAGTGA 60

QY 61 CAATCCGGTGAATATTACCGATCGCTGATGCCCTGGAGNTAAATGCCAAC 120

Db 61 CAATCCGGTGAATATTACCGATCGCTGATGCCCTGGAGNTAAATGCCAAC 120

QY 121 GACTATCCCT 131

Db 121 GACTATCCCT 131

RESULT 4
US-09-883-119A-21

Sequence 21 Application US/09/883/119A

Publication No. US20030104520A1
GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents

TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050

CURRENT APPLICATION NUMBER: US/09/883, 119A

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 22

LENGTH: 133

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: oligonucleotide

US-09-883-119A-22

Query Match 98.2%; Score 109; DB 9; Length 133;

Best Local Similarity 98.5%; Pred. No. 1.5e-29;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCAGTATAGGTGACTTATCTGTAATCTAAACGGGAACCTCTAGTGA 60

Db 1 GCGCAGTATAGGTGACTTATCTGTAATCTAAACGGGAACCTCTAGTGA 60

QY 121 GACTATCCCT 131

Db 121 GACTATCCCT 131

RESULT 5
US-09-883-119A-23

Sequence 23 Application US/09/883/119A

Publication No. US20030104520A1
GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents

TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids

FILE REFERENCE: 119927-1050

CURRENT APPLICATION NUMBER: US/09/883, 119A

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 129

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: oligonucleotide

US-09-883-119A-24

Query Match 81.7%; Score 107; DB 9; Length 129;

Best Local Similarity 80.5%; Pred. No. 8e-29;

Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCAGTATAGGTGACTTATCTGTAATCTAAACGGGAACCTCTAGTGA 60

Db 1 GCGCAGTATAGGTGACTTATCTGTAATCTAAACGGGAACCTCTAGTGA 60

QY 121 GACTATCCCT 131

Db 121 GACTATCCCT 131

Matches 129; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 ; OTHER INFORMATION: 'oligonucleotide
 QY 1 GCCTGAGTATAAGGTGACTTAACTGTAAACGGAACTCTCTAGTA 60
 ; Sequence 22, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIORITY FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 22
 ; LENGTH: 119
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide
 US-09-883-119A-22

RESULT 6
 Query Match 66.4%; Score 87; DB 9; Length 119;
 Best Local Similarity 90.8%; Pred. No. 1.3e-21; Mismatches 0; Indels 12; Gaps 2;
 Matches 119; Conservative 0; Mismatches 0; Indels 12; Gaps 2;
 QY 1 GCCTGAGTATAAGGTGACTTAACTGTAAACGGAACTCTCTAGTA 60
 ; Sequence 22, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIORITY FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 22
 ; LENGTH: 119
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide
 US-09-883-119A-22

RESULT 7
 US-09-883-119A-25
 ; Sequence 25, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIORITY FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 25
 ; LENGTH: 117
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide
 US-09-883-119A-25

RESULT 8
 US-09-883-119A-24
 ; Sequence 24, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIORITY FILING NUMBER: 60/212,097
 ; PRIORITY FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 24
 ; LENGTH: 115
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide
 US-09-883-119A-24

RESULT 9
 US-09-883-119A-30
 ; Sequence 30, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIORITY FILING NUMBER: US/09/883,119A
 ; PRIORITY FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 30
 ; LENGTH: 122
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide
 US-09-883-119A-30

Query Match 62.7%; Score 82.2; DB 9; Length 122;
 Best Local Similarity 83.2%; Pred. No. 6.8e-20; Mismatches 109; Conservative 0; Indels 9; Gaps 1;

Qy 1 GCCTGAGTATAAGGTGACTTAACTCTAAGGGAAACCTCTAGTAGA 60
 Dp 1 GCCTGAGTATAAGGTGACTTAACTCTAAGGGAAACCTCTAGTAGA 60
 Qy 61 CAATCCCGTGCTAAATTATACAGCATCTGCTTATGCCCTAAC 120
 Dp 61 CAATCCCGTGCTAAATTATACAGCATCTGCTTATGCCCTAAC 120
 Qy 121 GACTATCCT 131
 Db 112 GACTATCCT 122

RESULT 10
 US-09-883-119A-28
 Sequence 28, Application US/09883119A
 Publication No. US20030104520A1

GENERAL INFORMATION:
 APPLICANT: The University of Texas System Board of Regents
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 FILE REFERENCE: 119927-1050
 CURRENT APPLICATION NUMBER: US/09/883-119A
 PRIORITY FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: 60/212,097
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 28
 LENGTH: 107
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: oligonucleotide

US-09-883-119A-28

Query Match 62.1%; Score 81.4; DB 9; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.3e-19; Mismatches 104; Conservative 0; Indels 1; Gaps 2;

Qy 27 GATATCCTAAACGGGAACCTCTAGTAGACAATCCGGTCTAATT-ATACCGAC 85
 Db 1 GATATCCTAAACGGGAACCTCTAGACAATCCGGTCTAATT-ATACCGAC 60

Qy 86 ATCGCTCTGATGCCCTGGAG-ATTAATGCCCTAACGACTATCCCT 131
 Db 61 ATCGCTCTGATGCCCATGGCGCAATAACTCTAACGACTATCCCT 107

RESULT 11
 US-09-883-119A-16
 Sequence 16, Application US/09883119A
 Publication No. US20030104520A1

GENERAL INFORMATION:
 APPLICANT: The University of Texas System Board of Regents
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 FILE REFERENCE: 119927-1050
 CURRENT APPLICATION NUMBER: US/09/883-119A
 CURRENT FILING DATE: 2000-06-14
 PRIORITY FILING DATE: 2000-06-15
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 122
 TYPE: DNA
 FEATURE:
 OTHER INFORMATION: Parental P6 construct

US-09-883-119A-16

Query Match 61.5%; Score 80.6; DB 9; Length 122;
 Best Local Similarity 82.4%; Pred. No. 2.6e-19; Mismatches 108; Conservative 0; Indels 9; Gaps 1;

Qy 1 GCCTGAGTATAAGGTGACTTAACTCTAAGGGAAACCTCTAGTAGA 60
 Db 1 GCCTGAGTATAAGGTGACTTAACTCTAAGGGAAACCTCTAGTAGA 60
 Qy 61 CAATCCCGTGCTAAATTATACAGCATCTGCTTATGCCCTAAC 120
 Db 61 CAATCCCGTGCTAAATTATACAGCATCTGCTTATGCCCTAAC 120
 Qy 121 GACTATCCT 131
 Db 112 GACTATCCT 122

RESULT 12
 US-09-883-119A-29
 Sequence 29, Application US/09883119A
 Publication No. US20030104520A1

GENERAL INFORMATION:
 APPLICANT: The University of Texas System Board of Regents
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 FILE REFERENCE: 119927-1050
 CURRENT APPLICATION NUMBER: US/09/883-119A
 PRIORITY FILING DATE: 2000-06-14
 PRIOR FILING DATE: 2000-06-15
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 29
 LENGTH: 107
 TYPE: DNA
 FEATURE:
 OTHER INFORMATION: oligonucleotide

US-09-883-119A-29

Query Match 60.9%; Score 79.8; DB 9; Length 107;
 Best Local Similarity 96.3%; Pred. No. 4.7e-19; Mismatches 103; Conservative 0; Indels 2; Gaps 2;

Qy 27 GATATCCTAAACGGGAACCTCTAGTAGACAATCCGGTCTAATT-ATACCGAC 85
 Db 1 GATATCCTAAACGGGAACCTCTAGACAATCCGGTCTAATT-ATACCGAC 60

Qy 86 ATCGCTCTGATGCCCTGGAG-ATTAATGCCCTAACGACTATCCCT 131
 Db 61 ATCGCTCTGATGCCCATGGCGCAATAACTCTAACGACTATCCCT 107

RESULT 13
 US-09-883-119A-31
 Sequence 31, Application US/09883119A
 Publication No. US20030104520A1

GENERAL INFORMATION:
 APPLICANT: The University of Texas System Board of Regents
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 FILE REFERENCE: 119927-1050
 CURRENT APPLICATION NUMBER: US/09/883-119A
 CURRENT FILING DATE: 2000-06-14
 PRIORITY FILING DATE: 2000-06-15
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 31
 LENGTH: 124
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: oligonucleotide

US-09-883-119A-31

; OTHER INFORMATION: 'oligonucleotide
US-09-883-119A-26

Query Match 59.7%; Score 78.2; DB 9; Length 124;
 Best Local Similarity 80.9%; Pred. No. 1.9e-18;
 Matches 106; Conservative 0; Mismatches 18; Indels 7; Gaps 1;

QY 1 GCCGTAGTATAAGGAGCTATTAACGGGAACCTCTCTAGTAGA 60
 Db 1 GCCTGAGTATAAGGAGCTATTAACGGGAACCTCTCTAGTAGA 60

QY 61 CAATCCCGTCCTAAATTATACAGCATCTCTTGATGCCTTGCGAGATAARGCCTAC 120
 Db 61 CAATCCCGTCCTAAATTATACAGCATCTCTTGATGCCTTGCGAGATAARGCCTAC 113

QY 121 GACTATCCCT 131
 Db 114 GACTATCCCT 124

Search completed: July 13, 2003, 22:56:46
 Job time : 106 secs

; OTHER INFORMATION: 'oligonucleotide
US-09-883-119A-26

Query Match 37.9%; Score 49.6; DB 9; Length 144;
 Best Local Similarity 92.9%; Pred. No. 4.1e-08;
 Matches 52; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TGAGTATAAGGAGCTATTAACGGGAACCTCTCTAGTAG 59
 Db 1 TGAGTATAAGGAGCTATTAACGGGAACCTCTATACAG

RESULT 14
 US-09-883-119A-19

; Sequence 19, Application US/09883119A

; Publication No. US20030104520A1

GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 FILE REFERENCE: 119921-1050

CURRENT APPLICATION NUMBER: US/09/883,119A

CURRENT FILING DATE: 2000-06-14

PRIORITY APPLICATION NUMBER: 60/212,097

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 19

LENGTH: 94

TYPE: DNA

FEATURE: Artificial sequence

OTHER INFORMATION: oligonucleotide

US-09-883-119A-19

Query Match 58.0%; Score 76; DB 9; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGTAGTATAAGGAGCTATTAACGGGAACCTCTCTAGTAGA 60
 Db 1 GCCTGAGTATAAGGAGCTATTAACGGGAACCTCTCTAGTAGA 60

QY 61 CAATCCCGTCCTAAATTATACAGCATCTCTTGATGCCTTGCGAGATAARGCCTAC 120
 Db 61 CAATCCCGTCCTAAATTATACAGCATCTCTTGATGCCTTGCGAGATAARGCCTAC 113

RESULT 15

US-09-883-119A-26

; Sequence 26, Application US/09883119A

; Publication No. US20030104520A1

GENERAL INFORMATION:

APPLICANT: The University of Texas System Board of Regents
 TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 FILE REFERENCE: 119921-1050

CURRENT APPLICATION NUMBER: US/09/883,119A

CURRENT FILING DATE: 2000-06-14

PRIORITY APPLICATION NUMBER: 60/212,097

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 26

LENGTH: 144

TYPE: DNA

FEATURE: Artificial sequence

